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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/835,147

DATE: 04/30/2001

TIME: 09:22:54

Input Set : A:\2879-US 041201 Seq List.txt

Output Set: N:\CRF3\04302001\I835147.raw

ENTERED

3 <110> APPLICANT: Maliszewski, Charles R.
 4 Gayle III, Richard B.
 5 Price, Virginia L.
 6 Gimpel, Steven D.
 8 <120> TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
 10 <130> FILE REFERENCE: 2879-US
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/835,147
 C--> 13 <141> CURRENT FILING DATE: 2001-04-13
 15 <150> PRIOR APPLICATION NUMBER: US 60/104,585
 16 <151> PRIOR FILING DATE: 1998-10-16
 18 <150> PRIOR APPLICATION NUMBER: US 60/107,466
 19 <151> PRIOR FILING DATE: 1998-11-06
 21 <150> PRIOR APPLICATION NUMBER: US 60/149,010
 22 <151> PRIOR FILING DATE: 1999-08-13
 24 <150> PRIOR APPLICATION NUMBER: PCT/US99/22955
 25 <151> PRIOR FILING DATE: 1999-10-13
 27 <160> NUMBER OF SEQ ID NOS: 31
 29 <170> SOFTWARE: PatentIn Ver. 2.0
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 1599
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Homo sapiens
 36 <220> FEATURE:
 37 <221> NAME/KEY: CDS
 38 <222> LOCATION: (67)..(1596)
 40 <400> SEQUENCE: 1
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 43 ctactt atg gaa gat aca aag gag tct aac gtg aag aca ttt tgc tcc 108
 44 Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser
 45 1 5 10
 47 aag aat atc cta gcc atc ctt ggc ttc tcc tct atc ata gct gtg ata 156
 48 Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile
 49 15 20 25 30
 51 gct ttg ctt gct gtg ggg ttg acc cag aac aaa gca ttg cca gaa aac 204
 52 Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn
 53 35 40 45
 55 gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta 252
 56 Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu
 57 50 55 60
 59 tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg 300
 60 Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
 61 65 70 75
 63 cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt 348
 64 His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe
 65 80 85 90
 67 gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa 396
 68 Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu

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69	95		100		105		110	
71	aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt	444						
72	Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val							
73			115		120		125	
75	tac ctg gga gcc acg gca ggc atg cgg ttg ctc agg atg gaa agt gaa	492						
76	Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu							
77			130		135		140	
79	gag ttg gca gac agg gtt ctg gat gtg gtg gag agg agc ctc agc aac	540						
80	Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn							
81			145		150		155	
83	tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa	588						
84	Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu							
85			160		165		170	
87	ggt gcc tat ggc tgg att act atc aac tat ctg ctg ggc aaa ttc agt	636						
88	Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser							
89	175		180		185		190	
91	cag aaa aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag	684						
92	Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln							
93			195		200		205	
95	gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act	732						
96	Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr							
97			210		215		220	
99	ttt gta ccc caa aac cag act atc gag tcc cca gat aat gct ctg caa	780						
100	Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln							
101			225		230		235	
103	ttt cgc ctc tat ggc aag gac tac aat gtc tac aca cat agc ttc ttg	828						
104	Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu							
105			240		245		250	
107	tgc tat ggg aag gat cag gca ctc tgg cag aaa ctg gcc aag gac att	876						
108	Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile							
109	255		260		265		270	
111	cag gtt gca agt aat gaa att ctc agg gac cca tgc ttt cat cct gga	924						
112	Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly							
113			275		280		285	
115	tat aag aag gta gtg aac gta agt gac ctt tac aag acc ccc tgc acc	972						
116	Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr							
117			290		295		300	
119	aag aga ttt gag atg act ctt cca ttc cag cag ttt gaa atc cag ggt	1020						
120	Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly							
121			305		310		315	
123	att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac	1068						
124	Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn							
125			320		325		330	
127	acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg	1116						
128	Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu							
129	335		340		345		350	
131	cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg	1164						
132	Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val							
133			355		360		365	

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135 atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg 1212
136 Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
137          370          375          380
139 act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa 1260
140 Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
141          385          390          395
143 aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt 1308
144 Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
145          400          405          410
147 tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca 1356
148 Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr
149 415          420          425          430
151 gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc 1404
152 Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
153          435          440          445
155 gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc 1452
156 Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
157          450          455          460
159 cca gct gag caa cca ttg tcc aca cct ctc tcc cac tcc acc tat gtc 1500
160 Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val
161          465          470          475
163 ttc ctc atg gtt cta ttc tcc ctg gtc ctt ttc aca gtg gcc atc ata 1548
164 Phe Leu Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile
165          480          485          490
167 ggc ttg ctt atc ttt cac aag cct tca tat ttc tgg aaa gat atg gta 1596
168 Gly Leu Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val
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171 tag 1599
174 <210> SEQ ID NO: 2
175 <211> LENGTH: 510
176 <212> TYPE: PRT
177 <213> ORGANISM: Homo sapiens
179 <400> SEQUENCE: 2
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183 Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile Ala Leu
184          20          25          30
186 Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
187          35          40          45
189 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
190          50          55          60
192 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
193 65          70          75          80
195 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
196          85          90          95
198 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
199          100          105          110
201 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
202          115          120          125

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204 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
205 130 135 140
207 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
208 145 150 155 160
210 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
211 165 170 175
213 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
214 180 185 190
216 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
217 195 200 205
219 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
220 210 215 220
222 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
223 225 230 235 240
225 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
226 245 250 255
228 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
229 260 265 270
231 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
232 275 280 285
234 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
235 290 295 300
237 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
238 305 310 315 320
240 Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
241 325 330 335
243 Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
244 340 345 350
246 Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
247 355 360 365
249 Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
250 370 375 380
252 Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
253 385 390 395 400
255 Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
256 405 410 415
258 Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
259 420 425 430
261 Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
262 435 440 445
264 Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
265 450 455 460
267 Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu
268 465 470 475 480
270 Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu
271 485 490 495
273 Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val
274 500 505 510
277 <210> SEQ ID NO: 3

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278 <211> LENGTH: 476
279 <212> TYPE: PRT
280 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
283 <223> OTHER INFORMATION: Description of Artificial Sequence: Fusion
284 construct of human CD39
286 <400> SEQUENCE: 3
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290 Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
291 20 25 30
293 Ile Phe Leu Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
294 35 40 45
296 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
297 50 55 60
299 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
300 65 70 75 80
302 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
303 85 90 95
305 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
306 100 105 110
308 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
309 115 120 125
311 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
312 130 135 140
314 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
315 145 150 155 160
317 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
318 165 170 175
320 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
321 180 185 190
323 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
324 195 200 205
326 Phe Gly Ala Leu Asp Leu Gly Glu Ala Ser Thr Gln Val Thr Phe Val
327 210 215 220
329 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
330 225 230 235 240
332 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
333 245 250 255
335 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
336 260 265 270
338 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
339 275 280 285
341 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
342 290 295 300
344 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
345 305 310 315 320
347 Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
348 325 330 335

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

file://C:\CRF3\Outhold\Vsri835147.htm

4/30/01

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/835,147

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Input Set : A:\2879-US 041201 Seq List.txt
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L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:399 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

4/30/01

file://C:\CRF3\Outhold\VsrI835147.htm